Slobodyanska, 306-3222

1652 #11

CRF Errors Corrected by the STIC Systems Branch

Serial Number: 09/068,507A

CRF Processing Date: 2/18/99
Edited by: _____
Verified by: AV (STIC staff)

☐ Changed a file from non-ASCII to ASCII

☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.

☐ Edited a format error in the Current Application Data section, specifically: ENTERED

☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____.

☐ Added the mandatory heading and subheadings for "Current Application Data".

☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.

☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically:

_____

☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were:

_____

☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:

_____

☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.

☐ Inserted colons after headings/subheadings. Headings edited included:

_____

☐ Deleted extra, invalid, headings used by an applicant, specifically:

_____

☐ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as _____.

☐ Inserted mandatory headings, specifically: _____

☐ Corrected an obvious error in the response, specifically:

_____

☐ Edited identifiers where upper case is used but lower case is required, or vice versa.

☐ Corrected an error in the Number of Sequences field, specifically:

_____

☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.

☑ Deleted ***ending*** stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: 3, 5

☐ Other:

_____

_____

_____

_____

***Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.**

3/1/95

This Raw Listing contains the General Information Section and up to the first 5 pages.

SEQUENCE LISTING

(1) General Information:

(i) APPLICANT: EIJSINK, VINCENT G.H.
BRURBERG, MAY B.
NES, INGOLF F.

(ii) TITLE OF INVENTION: EXPRESSION SYSTEM IN MICROORGANISM AND ITS USE FOR EXPRESSING HETEROLOGOUS AND HOMOLOGOUS PROTEINS

(iii) NUMBER OF SEQUENCES: 12

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP
(B) STREET: PO BOX 747
(C) CITY: FALLS CHURCH
(D) STATE: VA
(E) COUNTRY: USA
(F) ZIP: 22040-0747

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: MURPHY JR., GERLAD M.
(B) REGISTRATION NUMBER: 28,977
(C) REFERENCE/DOCKET NUMBER: 1380-0122P

(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 703-205-8000
(B) TELEFAX: 703-205-8050

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: C-terminal

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Lactobacillus platarum
(B) STRAIN: C11

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

```
Lys Ser Ser Ala Tyr Ser Leu Gln Met Gly Ala Thr Ala Ile Lys Gln
1               5                  10                  15

Val Lys Lys Leu Phe Lys Lys Trp Gly Trp
            20                  25
```

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 114 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..114

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```
ATG ATG ATA TTT AAA AAA CTT TCA GAA AAA GAA TTG CAA AAA ATA AAC        48
Met Met Ile Phe Lys Lys Leu Ser Glu Lys Glu Leu Gln Lys Ile Asn
  1               5                  10                  15

GGT GGT ATG GCA GGA AAT AGT TCT AAT TTT ATT CAT AAG ATT AAA CAA        96
Gly Gly Met Ala Gly Asn Ser Ser Asn Phe Ile His Lys Ile Lys Gln
            20                  25                  30
```

```
100
101  ATT TTT ACC CAT CGT TAA                                              114
102  Ile Phe Thr His Arg  *
103           35
104
105
106  (2) INFORMATION FOR SEQ ID NO:3:
107
108         (i) SEQUENCE CHARACTERISTICS:
109               (A) LENGTH: 37 amino acids
110               (B) TYPE: amino acid
111               (D) TOPOLOGY: linear
112
113        (ii) MOLECULE TYPE: peptide
114
115        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
116
117  Met Met Ile Phe Lys Lys Leu Ser Glu Lys Glu Leu Gln Lys Ile Asn
118    1               5                  10                  15
119
120  Gly Gly Met Ala Gly Asn Ser Ser Asn Phe Ile His Lys Ile Lys Gln
121                20                  25                  30
122
123  Ile Phe Thr His Arg
124           35
125
126
127  (2) INFORMATION FOR SEQ ID NO:4:
128
129       (i) SEQUENCE CHARACTERISTICS:
130             (A) LENGTH: 186 base pairs
131             (B) TYPE: nucleic acid
132             (C) STRANDEDNESS: single
133             (D) TOPOLOGY: linear
134
135       (ii) MOLECULE TYPE: DNA (genomic)
136
137
138       (ix) FEATURE:
139             (A) NAME/KEY: CDS
140             (B) LOCATION: 1..186
141
142
143       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
144
145  ATG GAA AAG TTT ATT GAA TTA TCT TTA AAA GAA GTA ACA GCA ATT ACA        48
146  Met Glu Lys Phe Ile Glu Leu Ser Leu Lys Glu Val Thr Ala Ile Thr
147    1               5                  10                  15
148
149  GGT GGA AAA TAT TAT GGT AAC GGT GTA CAC TGT GGA AAA CAT TCA TGT        96
150  Gly Gly Lys Tyr Tyr Gly Asn Gly Val His Cys Gly Lys His Ser Cys
151                20                  25                  30
152
```

ACC GTA GAC TGG GGA ACA GCT ATT GGA AAT ATC GGA AAT AAT GCA GCT 144
Thr Val Asp Trp Gly Thr Ala Ile Gly Asn Ile Gly Asn Asn Ala Ala
35 40 45

GCA AAC TGG GCC ACA GGC GGA AAC GCT GGC TGG AAT AAA TAA 186
Ala Asn Trp Ala Thr Gly Gly Asn Ala Gly Trp Asn Lys *
50 55 60

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 61 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Glu Lys Phe Ile Glu Leu Ser Leu Lys Glu Val Thr Ala Ile Thr
1 5 10 15

Gly Gly Lys Tyr Tyr Gly Asn Gly Val His Cys Gly Lys His Ser Cys
20 25 30

Thr Val Asp Trp Gly Thr Ala Ile Gly Asn Ile Gly Asn Asn Ala Ala
35 40 45

Ala Asn Trp Ala Thr Gly Gly Asn Ala Gly Trp Asn Lys
50 55 60

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 82 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Promoter"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GAGTTCTTAA CGTTAATCCG AAAAAAACTA ACGTTAATAT TAAAAAATAA GATCCGCTTG 60

TGAATTATGT ATAATTTGAT TN 82

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 81 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Promoter"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CGCATATTAA CGTTTAACCG ATAAAGTTGA ACGTTAATAT TTTTTTTGCG CAGAAATGGT 60

AAATTGAAGC ATAATAGTCT N 81

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 82 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Promoter"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GCAGCATTAA CGTTAATTTT GATAAACGTA ACGTTAATGG ATAATCATCC TGTTTACAAA 60

TAGTGTATGA CATAATTAAG TN 82

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 81 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION *US/09/068,507A*

INPUT SET: S30728.raw

Line	Error	Original Text

Slobodyanskij

RAW SEQUENCE LISTING
PATENT APPLICATION *US/09/068,507A*

DATE: 02/18/1999
TIME: 13:50:38

INPUT SET: S30728.raw

This Raw Listing contains the General Information Section and up to the first 5 pages.

SEQUENCE LISTING

Does Not Comply
Corrected Diskette Needed

(1) General Information:

(i) APPLICANT: EIJSINK, VINCENT G.H.
BRURBERG, MAY B.
NES, INGOLF F.

(ii) TITLE OF INVENTION: EXPRESSION SYSTEM IN MICROORGANISM AND ITS USE FOR EXPRESSING HETEROLOGOUS AND HOMOLOGOUS PROTEINS

(iii) NUMBER OF SEQUENCES: 12

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP
(B) STREET: PO BOX 747
(C) CITY: FALLS CHURCH
(D) STATE: VA
(E) COUNTRY: USA
(F) ZIP: 22040-0747

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: MURPHY JR., GERLAD M.
(B) REGISTRATION NUMBER: 28,977
(C) REFERENCE/DOCKET NUMBER: 1380-0122P

(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 703-205-8000
(B) TELEFAX: 703-205-8050

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 38 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

```
Met Met Ile Phe Lys Lys Leu Ser Glu Lys Glu Leu Gln Lys Ile Asn
 1               5                  10                  15

Gly Gly Met Ala Gly Asn Ser Ser Asn Phe Ile His Lys Ile Lys Gln
            20                  25                  30

Ile Phe Thr His Arg *
        35
```

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 186 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..186

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```
ATG GAA AAG TTT ATT GAA TTA TCT TTA AAA GAA GTA ACA GCA ATT ACA      48
Met Glu Lys Phe Ile Glu Leu Ser Leu Lys Glu Val Thr Ala Ile Thr
 1               5                  10                  15

GGT GGA AAA TAT TAT GGT AAC GGT GTA CAC TGT GGA AAA CAT TCA TGT      96
Gly Gly Lys Tyr Tyr Gly Asn Gly Val His Cys Gly Lys His Ser Cys
            20                  25                  30

ACC GTA GAC TGG GGA ACA GCT ATT GGA AAT ATC GGA AAT AAT GCA GCT     144
Thr Val Asp Trp Gly Thr Ala Ile Gly Asn Ile Gly Asn Asn Ala Ala
        35                  40                  45

GCA AAC TGG GCC ACA GGC GGA AAC GCT GGC TGG AAT AAA TAA             186
Ala Asn Trp Ala Thr Gly Gly Asn Ala Gly Trp Asn Lys  *
    50                  55                  60
```

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 62 amino acids

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

```
Met Glu Lys Phe Ile Glu Leu Ser Leu Lys Glu Val Thr Ala Ile Thr
 1               5                  10                  15

Gly Gly Lys Tyr Tyr Gly Asn Gly Val His Cys Gly Lys His Ser Cys
            20                  25                  30

Thr Val Asp Trp Gly Thr Ala Ile Gly Asn Ile Gly Asn Asn Ala Ala
        35                  40                  45

Ala Asn Trp Ala Thr Gly Gly Asn Ala Gly Trp Asn Lys *
    50                  55                  60
```